



Biomarkers of particulate matter exposure in patients with chronic obstructive pulmonary disease: a systematic review

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Background: In recent years, ambient particulate matter (PM) exposure has been strongly linked with health effects. Elevated levels of PM in polluted air have been correlated with the onset and development of chronic obstructive pulmonary disease (COPD). This systematic review was conducted to evaluate biomarkers that could reflect the effects of PM exposure in patients with COPD.

Methods: We performed a systematic review of studies published on biomarkers associated with PM exposure in patients with COPD between January 01, 2012 and June 30, 2022 in PubMed/MEDLINE, EMBASE, and Cochrane databases. Studies that included data on biomarkers with COPD exposed PM were eligible for inclusion. Biomarkers were classified into 4 groups according to their mechanisms.

Results: Of the 105 studies identified, 22 were included in this study. Nearly 50 biomarkers have been proposed in the studies included in this review, and the most studied in relation to PM are several interleukins. Various mechanisms have been reported by which PM induces and aggravates COPD. Six studies related to oxidative stress, one related to direct effect of innate and adaptive immune systems, 16 associated with genetic regulation of inflammation, and two related to epigenetic regulation of physiology and susceptibility were found. Biomarkers related to these mechanisms were detected in serum, sputum, urine, exhaled breath concentration (EBC), and showed various correlations with PM in COPD.

Conclusions: Various biomarkers have shown potential in predicting the extent of PM exposure in COPD patients. Future studies are needed to establish recommendations for regulation to reduce airborne PM, which could be used to develop strategies for prevention and management of environmental respiratory diseases.

Keywords: Biomarker; particulate matter (PM); chronic obstructive pulmonary disease (COPD)

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Introduction

Chronic obstructive pulmonary disease (COPD) is a preventable disease associated with chronic pulmonary inflammation and remodeling induced by environmental exposures (1). The global socioeconomic impact of COPD

is substantial (2). According to the global health estimates by World Health Organization (WHO) in 2019, COPD was the third leading cause of death worldwide, accounting for 6% of all deaths (3). Although cigarette smoking is an important risk factor for COPD, it has been reported that

approximately 25–45% of patients with COPD have never smoked (4). Risk factors other than smoking currently account for more than 50% of the global burden of COPD (5). Thus, contributory factors linked to COPD other than smoking need to be considered.

In recent decades, air pollution has emerged as a major public health concern (6). Air pollutants include particulate matter (PM) and gaseous components, such as ozone, volatile organic compounds (VOCs), carbon monoxide, and nitrogen oxides. PM is a widespread air pollutant, consisting of a heterogeneous mixture of solid and liquid particles suspended in air (7). Common chemical constituents of PM include sulfate, nitrate, organic and elemental carbon, organic compounds, biological compounds, and heavy metals (8). Numerous scientific studies have shown that PM toxicity is linked to various respiratory diseases, such as asthma, COPD, idiopathic pulmonary fibrosis, and lung cancer (9–12).

Long-term exposure to PM increases the risk of development of COPD in the older population (13). The Global Burden of Disease Study in 2019 (14), reported that the absolute COPD burden attributed to PM_{2.5} (aerodynamic diameter $\leq 2.5 \mu\text{m}$) had greatly increased, and the older population was more vulnerable and bore more burden in line with an aging society. In addition, several epidemiologic studies have revealed that PM_{2.5} aggravates respiratory diseases by decreasing lung function (15), and

has also been associated with increased hospitalization, morbidity, and mortality related to COPD (16–18). PM is considered to play a role in COPD deterioration through a variety of mechanisms, including oxidative stress, inflammatory responses, inhibition of local airway immunity, and epigenetic alterations (19,20). However, there is paucity of evidence to determine biomarkers that would aid in identification of the causal relationship between COPD and PM exposure.

Therefore, we conducted this systematic review to gather data on mechanisms involved in the development and exacerbation of COPD by PM to evaluate putative biomarkers that could reflect the effects of PM exposure in patients with COPD. We present the following article in accordance with the PRISMA reporting checklist (available at <https://jtd.amegroups.com/article/view/10.21037/jtd-23-78/rc>) (21).

Methods

Eligibility criteria

The inclusion criteria were as follows: (I) population: patients with COPD; (II) intervention and comparator: PM (2.5, 10) exposure; (III) outcomes: biomarkers of PM exposure and their mechanisms in patients with COPD; (IV) studies published after 2012; and (V) full-text articles in English. The exclusion criteria were as follows: (I) studies that did not target patients with COPD, (II) studies that did not involve exposure to PM, (III) studies that did not report our outcomes of interest, and (IV) duplicated studies.

Information sources and search strategy

We searched the following electronic international databases (Ovid PubMed/MEDLINE, Ovid EMBASE, the Cochrane Central Register of Controlled Trials) on June 30, 2022 for studies published after January 01, 2012, to identify biomarkers of PM in COPD patients. The search strategy included the following combinations of keywords: (“particulate matter” OR “PM₁₀” OR “PM_{2.5}”) AND (“chronic obstructive pulmonary disease” OR “COPD”) AND (“biomarker” OR “Biomarkers”). Synonyms for PM were included using Medical Subject Heading (MeSH) terms and EMBASE subject headings (Emtree). The search was limited to studies published in English language. The search strategy is presented in [Appendix 1](#).

Highlight box

Key findings

- In this study, we searched literatures on relation between biomarkers and particulate matter (PM) exposure in patients with chronic obstructive pulmonary disease (COPD). We found that several biomarkers have various associations with PM exposure and have potential as predictors of development and exacerbation of COPD.

What is known and what is new?

- Various biomarkers were classified into four mechanisms in COPD patients exposed to PM. The most studied biological mechanism of biomarkers was related to genetic regulation of inflammation.
- This manuscript added significance of biomarkers to predict extent of PM exposure in patients with COPD.

What is the implication, and what should change now?

- This review will help establish preventive strategies for chronic respiratory diseases by identifying mechanism of clinical deterioration caused by PM in COPD patients and verifying available biomarkers.

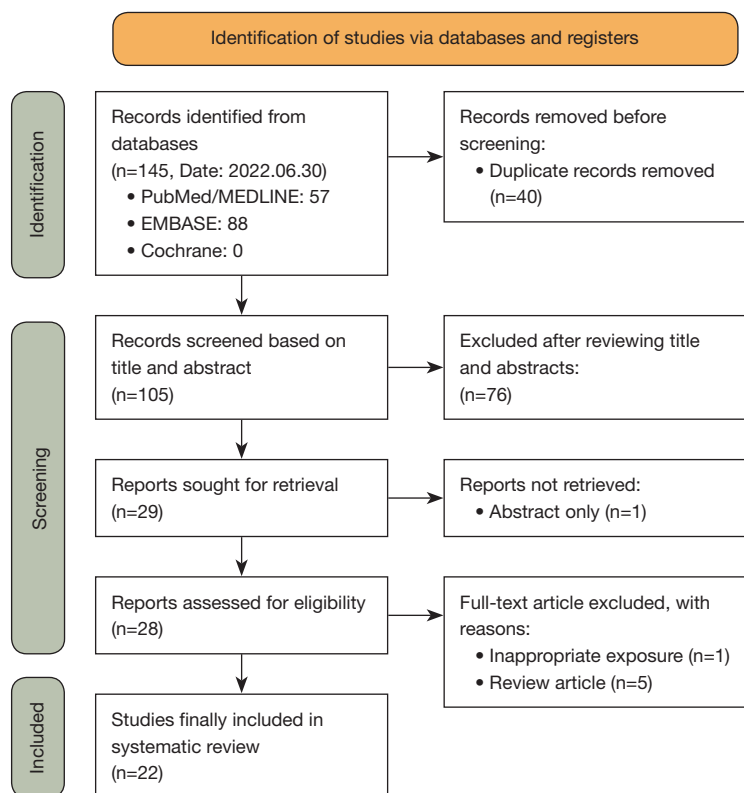


Figure 1 PRISMA flow diagram.

Selection process

Two authors (JK and NYK) screened the titles and abstracts for inclusion of studies. Each author independently assessed the eligibility of the identified studies, and conflicts were resolved by discussion. Full texts were assessed by two authors (JK and NYK) for final decision on inclusion or exclusion. Any disagreement between the two authors was resolved through discussion with a third author (WJK).

Data items and extraction

The following data were extracted from the eligible studies using an electronic spreadsheet (Microsoft Excel) of a pre-designed data extraction form: author, publication year, study design, study region, study setting, and study outcome. One author (NYK) extracted the data, and two other authors (JK and WJK) independently evaluated the data.

Study outcomes

The primary outcome was biomarkers of PM exposure and their mechanisms in patients with COPD.

Statistical analysis

In this study, no other statistical analysis was performed because of the lack of studies summarizing the risk of specific biomarkers. Instead, we fully reviewed the literature that was found through structurally searched results.

Results

Study selection and characteristics

A total of 145 studies were identified using the search strategy, and 40 duplicate studies were removed before screening. Of the 105 studies, 76 were excluded after screening the titles and abstracts. Subsequently, the full texts of 29 studies were reviewed. After reviewing the eligibility of the original articles, 22 studies were included (*Figure 1*). The list of excluded studies and reasons for exclusion are presented in [Table S1](#).

Most studies conducted repeated measures of exposure to ambient pollutants (PM or PM₁₀) and biomarkers (22-33), and panel studies (34-36). Other studies were performed by retrospective analysis of cross-sectional (37) or cohort

designs (38-43). Risk assumption according to primary and secondary outcomes could not be available due to heterogeneity in study outcomes and their reporting of the risk. Instead, in this review, we summarized the possible role of biomarkers linked to COPD according to four representative types of biological plausibility in patients with COPD exposed to PM through a qualitative review. Among 22 studies, six were found to be relevant regarding biomarkers exploring oxidative stress (22-24,37-39); one study investigated the roles of innate and adaptive immune systems (25); and 17 studies investigated genetic regulation (26-32,34-36,38-42) and epigenetic regulation of inflammation (27,43).

Biological mechanisms of biomarkers

Oxidative stress

Oxidative stress can be defined as damage resulting from imbalance of oxidation reaction and antioxidant reduction status of the body (44). In total, six original research articles reported an association between PM and oxidative stress biomarkers in patients with COPD (*Table 1*) (22-24,37-39). Human urinary metabolome, including 8-hydroxy-2'-deoxyguanosine (8-OHdG) and malondialdehyde (MDA) were found to positively correlate with PM exposure (22,23). Other PM_{2.5} related metabolic biomarkers such as uric acid, glyceric acid 1,3-biphosphate (GABP) and dopamine 4-sulfate were also found to be associated with COPD (37). In addition, Lee *et al.* (38) reported that elevated ubiquitin and beclin 1 levels were related to oxidative stress in COPD. Tang *et al.* (39) revealed that alteration of prothrombin time (PT) was associated with exacerbated COPD patients exposed to PM_{2.5}.

Direct effect of innate and adaptive immune system

Alveolar macrophages play an important role in clearing the airway by phagocytizing foreign debris, including PM. Exposure to PM stimulates innate and adaptive immune defenses in the respiratory system (45). One research paper related to the role of PM in stimulating innate and adaptive immunities was found through the systematic review (*Table 2*) (25). Belli *et al.* showed that elevated indoor PM_{2.5} was substantially correlated with elevated airway macrophage black carbon in a cohort of former smokers with COPD (Spearman's Rho =0.60, P=0.005). According to a multivariate longitudinal analysis, the total area of airway macrophage black carbon increased by 0.19 μm^2 for every 10 $\mu\text{g}/\text{m}^3$ rise in indoor PM_{2.5} (P=0.01). Authors

speculated that increased black carbon content derived from indoor PM exposure may result in dysfunctional macrophages and disruption of immune defense. These findings suggest that the amount of black carbon in alveolar macrophages may serve as an effective non-invasive biomarker of exposure to PM.

Genetic regulation of inflammation

Airway inflammation is a common pathophysiological mechanism through which air pollutants affect pulmonary diseases (40). A total of 16 articles that presented an association between PM and inflammatory biomarkers in patients with COPD were identified (*Table 3*).

The most frequently reported mechanism was genetic regulation of inflammation, and among them, various interleukins were the most studied entity in relation to PM (26,28-30,33,34,38,41). Eight published studies on several interleukins were included in this review. IL-6 was measured in seven studies and was the most extensively studied biomarker associated with air pollution in this review. Of the seven studies, four showed significant increase in IL-6 levels due to PM exposure (26,29,30,38), while one reported a significant decrease due to PM exposure (33). Two studies showed inconclusive association between IL-6 and PM exposure (28,41). In addition to IL-6, IL-2 (28), IL-12 (28), and IL-17A (28) showed positive correlations with PM, whereas IL-4 (28) and IL-13 (28,33) showed negative correlations. The relationship between PM and IL-8 has yielded inconsistent results in previous studies (28,33,34,41).

Five published studies used plasma C-reactive protein (CRP) as a biomarker, and it was reported that the circulating concentrations of CRP rose in response to inflammation (26,29,30,39,41). It has been generally reported that CRP increased significantly with PM exposure, but Dadvand *et al.* showed an inconclusive result between PM and CRP in COPD patients (41).

Fraction of exhaled nitric oxide (FeNO) is a well-validated noninvasive marker of airway inflammation caused by exposure to air pollution (46). Three published studies which assessed FeNO were included in this review (27,36,40), all of which demonstrated a positive association between PM and FeNO levels.

In addition, various other biomarkers, such as tumor necrosis factor α (TNF α) (28,33,34,41), circulating vascular cell adhesion molecule-1 (sVCAM-1) (26,29,30), fibrinogen (41), hepatocyte growth factor (41), ultrafine particle concentration in exhaled breath (42), and exhaled hydrogen sulfide (36).

Table 1 Characteristics of the included studies related to oxidative stress

Author, year	Study design	Location	Follow-up	Age, year [†]	Number	Pollutant	Biomarker	Sample	Outcome	Effect estimate
Grady <i>et al.</i> , 2018 (22)	Repeated measure (prospectively)	USA	2012.11–2014.12	72.7±8.4	82	PM _{2.5} , NO ₂	8-OHdG, MDA	Urine	Biomarkers	↑8-OHdG; ↑MDA
Huang <i>et al.</i> , 2018 (37)	Cross-sectional study	China	2016.3–2016.5	71.0±7.8	41	PM _{2.5}	Uric acid, GABP, Dopamine 4-sulfate	Urine	COPD-related metabolic biomarkers (vs. healthy control)	↓Uric acid; ↓GABP; ↓Dopamine 4-sulfate
Huang <i>et al.</i> , 2021 (23)	Repeated measure (prospectively)	USA	2012.11–2014.12	72.7±8.4	81	PM-gamma activities	8-OHdG, MDA	Urine	Biomarkers	↑8-OHdG; ↑MDA
Lee <i>et al.</i> , 2016 (38)	Repeated measure (from retrospective cohort)	Taipei	2013.01–2014.12	70.3±9.0	43	PM ₁₀	Ubiquitin, Beclin 1	Blood	Biomarkers, lung function	↑Ubiquitin; ↑Beclin 1
Tang <i>et al.</i> , 2021 (39)	Cross-sectional analysis (from retrospective cohort)	China	2017.03–2019.09	<65: 28.7%; >65: 71.3%	317	PM _{2.5}	PT	Blood	Markers, acute exacerbation of COPD (hospitalization)	↓PT
Manney <i>et al.</i> , 2012 (24)	Repeated measure (prospectively)	Finland, Greece, The Netherlands, UK	2002.10–2004.03	62.3±10.6	111	PM _{2.5} , PM ₁₀ , coarse particle, PNC	NOx	EBC	Biomarkers	No association

Statistically significant increase/decrease (↑/↓). [†], age is presented as mean ± standard deviation or percentage distribution. PM, particulate matter; NO₂, nitric dioxide; PNC, particle number concentration; 8-OHdG, 8-hydroxy-2'-deoxyguanosine; MDA, malondialdehyde; GABP, glyceric acid 1,3-bisphosphate; PT, prothrombin time; NOx, nitrogen oxides; EBC, exhaled breath concentration; COPD, chronic obstructive pulmonary disease.

Table 2 Characteristics of the included studies related to direct effect of innate and adaptive immune system

Author, year	Study design	Location	Follow-up	Age, year [†]	Number	Pollutant	Biomarker	Sample	Outcome	Effect estimate
Belli <i>et al.</i> , 2016 (25)	Repeated measure (prospectively)	USA	NA	67±4	20	PM _{2.5}	Airway macrophages black carbon content	Sputum	Biomarker	↑black carbon content

Statistically significant increase/decrease (↑/↓). [†], age is presented as mean ± standard deviation. NA, not applicable; PM, particulate matter.

Epigenetic regulation of physiology and susceptibility

Epigenetic changes are molecular changes that occur in DNA structure and gene expression due to methylation or acetylation of DNA, and these changes may mediate environmental effects on human health (44,47). We found two studies related to DNA methylation caused by exposure to air pollutants (Table 4). Chen *et al.* (27) suggested that some constituents of PM_{2.5} were significantly associated with a decrease in nitric oxide synthase isoform 2A methylation. Lee *et al.* (43) in their epigenome-wide association study identified that DNA methylation signals in blood were associated with long-term ambient air pollution exposure.

Discussion

In this review, the literature was systematically evaluated to identify biomarkers of COPD patients exposed to PM. This review did not include a meta-analysis because it was difficult to measure risk differences due to the heterogeneous outcomes of the studies. Nearly 50 biomarkers were suggested in the literature included in the review. We classified and organized the biomarkers of COPD patients exposed to PM into four mechanisms.

COPD remains the most common cause of chronic disease-attributable deaths (48), however, there has been no significant progress in its treatment or prevention. To prevent some types of COPD, the Lancet Commission recently classified COPD into five types: genetics, early life events, pulmonary infections, tobacco smoke exposure, and air pollution, and emphasized the possibility of early intervention and prevention (49). The proposed novel classification results from heterogeneity, which contributes to the clinical presentation of COPD (50). The putative pathophysiologic mechanisms implicated in COPD in never-smokers include inflammation, oxidative stress, airway remodeling, and airflow limitation (5).

Several cohort studies have demonstrated that PM

is associated with mortality and morbidity in chronic respiratory diseases (20,44,51). Although the toxicological mechanism is still not fully understood, numerous studies in recent years have indicated that oxidative stress is the major mechanism by which toxicity can be exerted (20,52,53). Oxidative stress develops when production of reactive oxygen species (ROS) and antioxidant defense are unbalanced, and redox homeostasis is disrupted (54). Grady *et al.* (22) and Huang *et al.* (23) showed that ambient PM concentration had a significant positive association with urinary surrogate markers of oxidative stress such as 8-OHdG and MDA. Since urinary 8-OHdG is formed due to hydroxyl radical attack on DNA, it is used to evaluate the extent of DNA damage repair caused by ROS (55). In addition, urinary MDA is an end product of fatty acid oxidation, and can be used to estimate the extent of lipid peroxidation (56). A prospective cohort study assessed the relationship between indoor black carbon exposure and urinary oxidative stress biomarkers, 8-OHdG and MDA in participants with COPD. The authors reported a positive association between black carbon exposure and 8-OHdG and MDA, suggesting that exposure to air pollution resulted in lipid peroxidation and oxidative DNA damage in patients with COPD. These positive effects were most prominent on the day before urine collection (6.9% increase per interquartile range) for 8-OHdG and 1–4 days before collection (8.3% increase per interquartile range) for MDA (22). In contrast, uric acid, GABP, and dopamine 4-sulfate are metabolic intermediates in glycolysis and negative metabolites (37).

Chronic airway inflammation is involved in the pathogenesis of COPD, and several studies have been conducted to identify biomarkers to predict COPD changes due to inflammation (57–59). A previous meta-analysis suggested that COPD was associated with systemic inflammation characterized by leukocytosis and increased CRP, IL-6, IL-8, and fibrinogen levels (60). Moreover,

Table 3 Characteristics of the included studies related to genetic regulation of inflammation

Author, year	Study design	Location	Follow-up	Age, year [†]	Number	Pollutant	Biomarker	Sample	Outcome	Effect estimate
Abramson et al., 2020 (40)	Cross-sectional analysis (from retrospective cohort)	Germany	1985–1994	74.6±2.6	236	PM _{2.5}	FeNO	EBC	Biomarker	↑FeNO
Audi et al., 2017 (33)	Repeated measure (prospectively)	France	1st phase: 2009–2010; 2nd phase: 2011–2012	47.02±10.1	72	PM _{2.5} , VOCs	IL4, IL5, IL6, IL8, IL10, IL13, IL17, IFN γ , TNF α	Blood	Biomarkers	↓IL4, IL6, IL8, IL13, IFN γ , TNF α
Busenkell et al., 2022 (26)	Repeated measure (prospectively)	USA	2012.11–2017.5	72.9±8.3	144	PM _{2.5} , black carbon	CRP, IL6, sVCAM-1	Blood	Biomarkers	↑CRP (non-statin users); ↑IL6 (non-statin users); sVCAM-1: no association
Chen et al., 2015 (27)	Repeated measure (prospectively)	China	2013.9–2013.12	64±8	30	PM _{2.5}	FeNO	EBC	Biomarker	↑FeNO
Chen et al., 2021 (34)	Panel study	China	Enrolled from May 2016, 2–4 follow-up visits	61±8	53	PM _{2.5}	IL8, TNF α	Blood	Biomarkers (vs. healthy control)	↑time difference of IL8, TNF α (vs. healthy control)
Dadvand et al., 2014 (41)	Cross-sectional analysis (from retrospective cohort)	Spain	2004.1–2006.3	67.8±8.6	251	PM _{2.5} , NO ₂	CRP, TNF α , IL6, IL8, fibrinogen, HGF	Blood	Biomarkers	PM _{2.5} : not conclusive; NO ₂ : ↑CRP, IL8, fibrinogen, HGF
Gao et al., 2020 (28)	Repeated measure (prospectively)	China	2015.12–2017.9	63.9±6.3	84	PM _{2.5} , PM ₁₀ , NO ₂ , SO ₂ , CO, O ₃	IL1 β , IL2, IL4, IL5, IL6, IL8, IL10, IL12P70, IL13, IL17A, TNF α , IFN γ , VEGF-A, MCP-1, IP10, GM-CSF, sCD40L, MIP, Eotaxin	Blood	Biomarkers, lung function	↓Eotaxin, IL4, IL13 ↑IL2, IL12, IL17A, IFN γ , MCP-1, sCD40L
Garshick et al., 2018 (29)	Repeated measure (prospectively)	USA	2012.11–2014.12	72.7±8.4	88	Indoor black carbon	IL6, CRP, sVCAM-1	Blood	Biomarkers	↑CRP; ↑IL6 (non-statin users); sVCAM-1: no association
Huang et al., 2020 (30)	Repeated measure (prospectively)	USA	2012.10–2014.12	72.7±8.6	85	PM-gamma activities	CRP, IL6, sVCAM-1	Blood	Biomarkers	↑CRP, IL6; sVCAM-1: no association

Table 3 (continued)

Table 3 (continued)

Author, year	Study design	Location	Follow-up	Age, year [†]	Number	Pollutant	Biomarker	Sample	Outcome	Effect estimate
Fireman Klein et al., 2020 (42)	Cross-sectional analysis (from prospective design)	Israel	NA	68.3±8.6	58	PM _{2.5}	Ultrafine particles	EBC	Biomarkers (vs. healthy control)	↓Ultrafine particles
Lee et al., 2016 (38)	Cross-sectional analysis (from retrospective cohort)	Taipei	2013.01–2014.12	70.3±9.0	43	PM ₁₀	RAGE, IL6	Blood	Biomarkers	↑RAGE; ↑IL6
Lee et al., 2015 (31)	Repeated measure (prospectively)	Taipei	2013.01–2014.08	70.7±8.4	50	PM ₁₀	ITIH4, PRG4, APOF	Blood	Biomarkers (vs. healthy control)	↓ITIH4
Nurhussien et al., 2022 (32)	Repeated measure (prospectively)	USA	2017.02–2019.01	71.1±8.4	30	PM _{2.5} , NO ₂ , O ₃	blood eosinophil count	Blood	Biomarker, lung function	PM _{2.5} , NO ₂ : ↓FEV ₁ (BEC >150)
Pirozzi et al., 2015 (35)	Panel study	USA	2012.12–2013.03	40–85	16	PM _{2.5}	NOx, 8-isoprostane	EBC	Biomarkers, symptoms	↑NOx; 8-isoprostane: no association
Tang et al., 2021 (39)	Cross-sectional analysis (from retrospective cohort)	China	2017.03–2019.09	<65: 28.7%; >65: 71.3%	317	PM _{2.5}	CRP	Blood	Biomarker	↑CRP
Wu et al., 2016 (36)	Panel study	China	Period 1: 2014.1–2014.4; Period 2: 2014.8–2014.9	Period 1: 73.6±4.7; Period 2: 74.8±3.4	25	PM _{2.5} , PM ₁₀ , NO ₂ , SO ₂	FeNO, Exhaled H ₂ S	EBC	Biomarker, symptoms	↑FeNO

Statistically significant increase/decrease (↑/↓). [†] age is presented as mean ± standard deviation, range or percentage distribution. NA, not applicable; PM, particulate matter; VOC, volatile organic compound; NO₂, nitric dioxide; FeNO, fractional exhaled nitric oxide; IL, interleukin; IFN γ , interferon gamma; TNF α , tumor necrosis factor α ; CRP, C reactive protein; sVCAM-1, circulating vascular cell adhesion molecule-1; HGF, hepatocyte growth factor; VEGF-A, vascular endothelial growth factor A; MCP-1, monocyte displacing protein 1; IP10, interferon gamma-induced protein; GM-CSF, granulocyte-macrophage colony stimulating factor; sCD40L, soluble CD40 ligand; MIP, macrophage inflammatory protein; RAGE, receptor for advanced glycation end-products; ITIH4, inter-alpha-trypsin inhibitor heavy chain 4; PRG4, proteoglycan 4; APOF, apolipoprotein F; NOx, nitrogen oxides; H₂S, hydrogen sulfide; EBC, exhaled breath concentration; FEV₁, forced expiratory volume in the first second; BEC, blood eosinophil count.

Table 4 Characteristics of the included studies related to epigenetic regulation of physiology and susceptibility

Author (year)	Study design	Location	Follow-up	Age, year [†]	Number	Pollutant	Biomarker	Sample	Outcome	Effect estimate
Chen <i>et al.</i> , 2015 (27)	Repeated measure (prospectively)	China	2013.9–2013.12	64±8	30	PM _{2.5}	NOS2A methylation	Blood	Biomarker	↓methylation of NOS2A
Lee <i>et al.</i> , 2019 (43)	Cross-sectional analysis (from prospective design)	Korea	NA	72.8±6.3	100	PM ₁₀ , NO ₂	Methylated CpGs	Blood	Biomarker	Variable effects

Statistically significant increase/decrease (↑/↓). [†], age is presented as mean ± standard deviation. NA, not applicable; PM, particulate matter; NO₂, nitric dioxide; NOS2A, nitric oxide synthase isoform 2A; CpG, C-phosphate-G.

association between systemic inflammatory markers and PM has been widely assessed (61,62). Much of the evidence in this review suggested that interleukins were potential predictors of PM exposure. The seven studies included in this review showed that IL-6 levels exhibited various associations with PM exposure. This might be related to the characteristics of IL-6, which acts as both anti-inflammatory and proinflammatory cytokine (63). Another well-known inflammatory marker, CRP, is a highly sensitive systemic marker of inflammation and tissue damage, which is well-standardized, reproducible, and readily available (64). CRP consistently showed a statistically significant positive association with extent of PM exposure in four CRP-measuring studies which were included in this review (26,29,30,39). Another well-studied systemic marker was FeNO level. Measurement of FeNO is a non-invasive method that rules in asthma, and facilitates the determination of inhaled corticosteroid responsiveness, making it convenient for application in primary care clinics (65). Several epidemiological studies have shown that FeNO is positively linked with PM (66,67). Further research is needed to predict PM exposure using minimally invasive methods to enable early intervention in COPD.

Moreover, air pollutants are known to generate ROS, and oxidative DNA damage can prevent methyltransferases from interacting with DNA, resulting in hypomethylation of cytosine residues at CpG sites (47). Several studies have shown that PM also induces histone modifications that aids in the expression of several inflammatory genes (68,69). One of the studies included in this review by Chen *et al.* showed that some specific components of PM might be associated with decreased methylation in COPD patients (27). These epigenetic changes are inextricably associated with inflammation and oxidative stress. Thus, oxidative stress,

inflammation, and epigenetic changes are intimately linked (70), and play significant roles in the pathophysiology of COPD.

Although rare, the direct effect of innate and adaptive immune system mechanisms can also be explained as one of the PM-induced mechanisms in patients with COPD. The inhalation of noxious particles is mainly removed by the mucociliary escalator in the tracheobronchial area, but relatively small particles get deposited in the alveolar space (71). Alveolar macrophages play an important role in clearing and processing these fine particles via scavenger and toll-like receptors, and also activate innate and adaptive immune responses (45). Commuting to work by bicycle was found to be related to the inhaled dose of black carbon in a previous study in London. Airway macrophage carbon was detected more frequently in cyclists compared to non-cyclists (72). Consistent with a previous study (72), Belli *et al.* showed that higher indoor PM_{2.5} was significantly associated with an increase in black carbon of airway macrophages in patients with COPD (0.19 μm² increase per 10 μg/m³ indoor PM_{2.5}) (25).

Several airway biomarkers have been proposed to establish strategies for diagnosis and prevention of diseases caused by air pollutants. However, measuring biomarkers related to PM exposure is a challenging task because exposure is usually chronic, with low to moderate exposure levels over long periods of time (73). In addition, it was found that the effect estimates of PM exposure showed various associations with use of single surrogate biomarkers. The ECLIPSE study (74), which defined subtypes of COPD and explored novel biomarkers, used a combined panel of six serum inflammatory markers to compare systemic inflammation between smokers with normal lung function and smokers with COPD. They showed that the mortality

of participants with persistent systemic inflammation was six times higher than that of participants without inflammation. Certain biomarkers may be more useful in combination with other markers in determining the effects of exposure to air pollution on COPD (62). Further research is needed to predict the disease prognosis of COPD patients exposed to PM using a combination of various biomarkers to validate future therapeutic interventions.

Our study had few limitations. First, this study did not perform a meta-analysis because most of the outcomes were biomarkers, and risk summation could not be performed. Second, most studies analyzed the relationship between a single biomarker and PM, and confounding factors that could affect the biomarker could not be quantified. Third, the available literature lacks longitudinal studies that investigated the temporal relationship between biomarkers and PM.

Conclusions

This systematic review summarized the available literature on the relationship between PM and biomarkers in patients with COPD. We verified several systemic biomarkers that were significantly associated with PM exposure. It was observed that epigenetic regulation of inflammation was the most studied entity, but the use of biomarker for monitoring COPD patients exposed to PM is still not enough evidence. Future studies are needed to establish recommendations for regulation to reduce airborne PM, which could be used to develop strategies for prevention and management of environmental respiratory diseases.

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